

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 05:12:55 ; Search time 1602.78 Seconds  
(without alignments)  
9027.275 Million cell updates/sec

Title: US-09-811-118-2

Perfect score: 1072  
Sequence: 1 GACGCCGCGACACTCGCGAAC.....TTGCATCCACATGATTTTC 1072

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapept 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estl:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	621	57.9	1011	9	AL543692 AL543692
2	577	53.8	961	9	AL543655 AL543655
3	553	51.6	936	10	BI905842 BI905842
4	531	49.5	760	10	BI550170 BI550170
5	524	46.9	625	9	AW957082 AW957082
6	502	46.8	617	10	BE383506 BE383506
7	468	43.7	519	9	AA406605 AA406605
8	465	43.4	534	10	BE314194 BE314194
9	452	43.2	466	9	AI635816 AI635816
10	452	43.2	466	9	AL554204 AL554204
11	437	40.8	846	10	BI561449 BI561449
12	419	39.1	465	9	AI925364 AI925364
13	409	38.2	464	9	AW576111 AW576111
14	404	37.7	456	9	AA599283 AA599283
15	400	37.3	466	9	AI332841 AI332841
16	399	37.2	436	9	AA557291 AA557291
17	388	36.2	894	10	BI767772 BI767772

C 18	370	34.5	382	9	AW195935	AW195935	xl85a05.x
C 19	351	32.7	397	9	AI376136	AI376136	ta59c04.x
C 20	349	32.6	436	9	AI094047	AI094047	qa28f09.s
C 21	347	32.4	367	9	AA722806	AA722806	zg81g08.s
C 22	346	32.3	403	9	AA405247	AA405247	UI-HF-BL0
C 23	340	31.7	450	9	AA815259	AA815259	a164d10.s
C 24	339	31.6	453	9	AI093865	AI093865	qa30e01.s
C 25	338	31.5	426	9	AA778372	AA778372	z156b05.s
C 26	337	31.4	399	9	AA736389	AA736389	x015e01.x
C 27	330	30.8	524	10	BE856755	BE856755	7f68c12.x
C 28	328	30.6	447	9	AI199140	AI199140	q146f11.x
C 29	327	30.5	327	9	BE047114	BE047114	hq64g08.x
C 30	327	30.5	454	10	BE646653	BE646653	7e91h09.x
C 31	325	30.3	419	9	AA777994	AA777994	z4f4c03.s
C 32	321	29.9	423	10	WA7086	WA7086	zc43e03.r1
C 33	314	29.3	405	10	BR110030	BR110030	7n45b05.x
C 34	312	29.1	366	9	AM135756	AM135756	UI-H-BL1
C 35	310	28.9	542	9	AA959644	AA959644	EST371714
C 36	296	27.6	435	9	AA749209	AA749209	ny11h09.s
C 37	239	22.3	435	9	AA992639	AA992639	ot81b11.s
C 38	232	21.6	356	9	AI401448	AI401448	t664b11.x
C 39	227	21.2	720	10	BT772530	BT772530	60305444
C 40	217	20.2	390	10	BS900356	BS900356	HOA37-1-G
C 41	216	20.1	392	10	BS900355	BS900355	HOA37-1-G
C 42	210	19.6	411	9	AA700564	AA700564	z134b10.s
C 43	200	18.7	331	9	AA975019	AA975019	on59e06.s
C 44	195	18.2	238	9	AA592186	AA592186	hf47c06.x
C 45	194	18.1	465	9	AI312116	AI312116	qp89c08.x

## ALIGNMENTS

RESULT 1  
AL543692  
LOCUS AL543692 1011 bp mRNA linear EST 16-FEB-2001  
DEFINITION AL543692 LTR\_NFL006.PL2 Homo sapiens CDNA clone CS0DDI006YD22 5  
prime, mRNA sequence.  
ACCESSION AL543692  
VERSION AL543692.1 GI:12876171  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 1011)  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
source  
1. 1011  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DDI006YD22"  
/clone\_1lb="LTR\_NFL006.PL2"  
/ribose\_type="piacenta"  
/note="Vector: PCMVSPORT 6; Site\_1: NotI; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded CDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 251 a 279 c 262 g 217 t 2 others  
ORIGIN



Oy	936	TGTGAGATTAGATGAATAACCTGGAAAGCGCTAGGCACATTCGCCAATATGAGAG	995
Db	226	TGTGAGATTAGATGAANTACTTGTAAGTGGCCTAGGCACTGGCCAAATATGAGAG	167
Oy	996	CATTCAATGAACATTTTGTGCATATATAA	1023
Db	166	CATTCAATGAACATTTTGTGCATATATAA	139
RESULT	3		
Bt905842			
LOCUS	Bt905842	936 bp	mRNA linear EST 16-OCT-2001
DEFINITION	603062920P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212085 5',		
ACCESSION	Bt905842		
VERSION	Bt905842.1	GI:16166433	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 936)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLM11532 row: h column: 06 High quality sequence start: 5 High quality sequence stop: 861. Location/Qualifiers		
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source	1..936		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_image="IMAGE:5212085"		
	/clone_id="NIH_MGC_118"		
	/tissue_type="Leukocyte"		
	/lab_host="DH10B"		
	/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."		
BASE COUNT	220 a 268 c 248 g 200 t		
ORIGIN			
Query Match	51.6%; Score 553; DB 10; Length 936;		
Best Local Similarity	99.6%; Pred. No. 2.6e-274;		
Matches 703; Conservative	0; Mismatches 3; Indels 0; Gaps 0;		
Oy	13	TCCGGAACAAGCATGGGCGGCGAGCGGTGCACGGCGTGGCTTCCTGGGGCTGC	72
Db	9	TCCGGAACAAGCATGGTGGCGGCGACGGTGCACGGCGGTGGCTCTCTGTGGGCTGC	68
Oy	73	GGCCTGCGCGCAGCAGCAGACGACTTACACTTCAAGCGCGTCAACATCCGGGGCAA	132
Db	69	GGCCTGCGCGCAGCAGCAGACGACTTACACTTCAAGCGCGTCAACATCCGGGGCAA	128
Oy	133	ACTGCTGTGCTGTGAAGAAGTACC GGCGATCGGTGTTCCTGTGGTGAATGTGGCCAAGCA	192

Db	129	ACTGCTGTGCTGGAGAAAGTACCGGGGAAATGGGTGTCCTCCGCGTGGTGGAAATGTGCCAGGCA	188
QY	193	GTGCGGCTTCAACAGACCAAGCACTACCGAGCCCTGCAGACAGCTGCAGACGCAAGACCTGGGCC	252
Db	189	GTGCGGCTTCAACAGACCAAGCACTACCGAGCCCTGCAGACAGCTGCAGACGCAAGACCTGGGCC	248
QY	253	CCACCACTTCAACAGCTGCTGCTCCCTCCGCAACCAAGTTTGGCCCAAGAGACCTGCACAG	312
Db	249	CCACCACTTCAACAGCTGCTGCTCCCTCCGCAACCAAGTTTGGCCCAAGAGACCTGCACAG	308
QY	313	CAACAAAGAGATTGAGAGCTTTGCTGCCGCAACCTACAGTGTCTCATTTCCCATGTTAG	372
Db	309	CAACAAAGAGATTGAGAGCTTTGCTGCCGCAACCTACAGTGTCTCATTTCCCATGTTAG	368
QY	373	CAAGATTGAGTACACCGGATGCTGAGGCCATCTGCTCAGTACCTGACCTGGCCCAACATTC	432
Db	369	CAAGATTGAGTACACCGGATGCTGAGGCCATCTGCTCAGTACCTGACCTGGCCCAACATTC	428
QY	433	TGGGAAGAGAGCCCACTGGAACTTTGTGAAGTACCTAGTAGGCCCAAGATGAAAGTGTG	492
Db	429	TGGGAAGAGAGCCCACTGGAACTTTGTGAAGTACCTAGTAGGCCCAAGATGAAAGTGTG	488
QY	493	AGGGCTTTGGAGCCCACTGTCTCAGTGTGAGAGAGGTCAAGCTCCAGATTCACAGCCCTGT	552
Db	489	AGGGCTTTGGAGCCCACTGTCTCAGTGTGAGAGAGGTCAAGCTCCAGATTCACAGCCCTGT	548
QY	553	GAGGAAGCTCATCTACTGTGAAGCGAGAAGACTTATACACAGCCGCTCTCTCTCACCA	612
Db	549	GAGGAAGCTCATCTACTGTGAAGCGAGAAGACTTATACACAGCCGCTCTCTCTCACCA	608
QY	613	CCTCATCCCGCCCACTGTGTGGGCTGACCAATGCAAATCTCAATGTGCTTCAAGGG	672
Db	609	ACTCATCCCGCCCACTGTGTGGGCTGACCAATGCAAATCTCAATGTGCTTCAAGGG	668
QY	673	AGAGACCCCACTGCTCTCTCTTCTTACGCTATGACATTTGGTCCC	718
Db	669	AGAGACCCCACTGCTCTCTCTTCTTACGCTATGACATTTGGTCCC	714
RESULT	4		
LOCUS	BI550170	760 bp	linear EST 05-SEP-2001
DEFINITION	603193057P1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5264151 5',		
ACCESSION	BI550170		
VERSION	BI550170.1	GI:15437482	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Carnivora; Catarrhini; Hominoidea; Homo.		
TITLE	1 (bases 1 to 760)		
JOURNAL	NIH-MGC <a href="http://mhc.nci.nih.gov/">http://mhc.nci.nih.gov/</a> .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: L14M1166 row: a column: 16 High quality sequence stop: 750. Location/Qualifiers 1. 760 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5264151" /clone_11b="NIH_MGC_95"		
FEATURES			
SOURCE			

/tissue\_type="hippocampus"  
/lab\_host="DH108"  
/note="Organ: brain; Vector: pBluescript (modified  
pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag  
); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTVN-3',  
size-selected for average insert size 2.5 kb and  
normalized to R0T 5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NIH/NHGRI, National  
Institutes of Health). Note: This is a NIH\_MGC Library."  
BASE COUNT 160 a 237 c 214 g 149 t  
ORIGIN

Query Match 49.5%; Score 531; DB 10; Length 760;  
Best Local Similarity 99.7%; Pred. No. 6e-263;  
Matches 631; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGCGCACCTCGGAAACAGCATGTTGGCGGAGCGGCGGCGGTGCTGCT 60  
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DB 20 GAGCGCGCACCTCGGAAACAGCATGTTGGCGGAGCGGCGGCGGTGCTGCT 79  
|||||  
QY 61 CCTGTGGCTGGCGGCTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
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DB 80 CCTGTGGCTGGCGGCTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 139  
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QY 121 CATCGGCGGAG 180  
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DB 140 CATCGGCGGAG 199  
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QY 181 TGTGGCCAG 240  
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DB 200 TGTGGCCAG 259  
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QY 241 AGAGCTGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
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DB 260 AGAGCTGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319  
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QY 301 GAGGCGTGCAG 360  
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DB 320 GAGGCGTGCAG 379  
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QY 361 CCCCATGTTTACAGAGATTCAGATCCGCTGCTGCTGCTGCTGCTGCTGCT 420  
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DB 380 CCCCATGTTTACAGAGATTCAGATCCGCTGCTGCTGCTGCTGCTGCTGCT 439  
|||||  
QY 421 GCGCCAGAGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
|||||  
DB 440 GCGCCAGAGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 499  
|||||  
QY 481 TGGAAAGGTGTAGAGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
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DB 500 TGGAAAGGTGTAGAGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 559  
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QY 541 CACAGCGCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
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DB 560 CACAGCGCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 619  
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QY 601 CCTCTCCACAG 633  
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DB 620 CCTCTCCACAG 652  
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RESULT 5  
AM957082 AM957082 625 bp mRNA linear EST 01-JUN-2000  
LOCUS  
DEFINITION EST369152 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.  
ACCESSION AM957082  
VERSION AM957082.1 GI:8146765  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt  
, I.E., Sneed, A.L., Sharov, V., Lee, N.H., Yeatman, T.J. and  
Quackenbush, J.  
TITLE  
Assessment of gene expression patterns in a model of colon tumor  
metastasis using a 19,200 element cDNA microarray  
JOURNAL  
Unpublished (2000)  
COMMENT  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: johng@tigr.org  
Plate: 101  
Seq primer: Reverse.

FEATURES  
source  
Location/Qualifiers  
1..625

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="MAGE resequences, MAGD"  
/note="Vector: pBluescriptSM"  
BASE COUNT 200 a 150 c 127 g 147 t 1 others  
ORIGIN

Query Match 48.9%; Score 524; DB 9; Length 625;  
Best Local Similarity 100.0%; Pred. No. 2.4e-259;  
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 535 CCAGATACAGCGCTCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 594  
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DB 22 CCAGATACAGCGCTCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 81  
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QY 595 GCGTCCTCTCTCCAG 654  
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DB 82 GCGTCCTCTCTCCAG 141  
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QY 655 AATAGTGCTTAAAG 714  
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DB 142 AATAGTGCTTAAAG 201  
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QY 715 TCCCATCATCTTGTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774  
|||||  
DB 202 TCCCATCATCTTGTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261  
|||||  
QY 775 AATAGAGAGCTCGTGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 834  
|||||  
DB 262 AATAGAGAGCTCGTGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 321  
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QY 835 TCTTGGCAACAAAATGTGTGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 894  
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DB 322 TCTTGGCAACAAAATGTGTGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 381  
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QY 895 GCTTGTGTAACTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 954  
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DB 382 GCTTGTGTAACTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441  
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QY 955 TACCTGTGAAGAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014  
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DB 442 TACCTGTGAAGAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501  
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RESULT 6  
BE383506 BE383506 617 bp mRNA linear EST 21-JUL-2000  
LOCUS  
DEFINITION 601298586F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3628580 5',  
mRNA sequence.

Accession	Version	KeyWords	Source	Organism	Reference	Authors	Title	Journal	Comment
BE383506	1	GI:9328871	EST	human.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (Bases 1 to 617)	NIH-MGC <a href="http://imgc.ncl.nih.gov/">http://imgc.ncl.nih.gov/</a>	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabs-r@mail.nih.gov">cgabs-r@mail.nih.gov</a> Tissue Procurement: ATCC
CDNA Library	Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Incyte Genomics, Inc.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">image.llnl.gov</a>	Plate: LCMW13	row: 1	column: 21	High quality sequence start: 7	High quality sequence stop: 617.	Location/Qualifiers
FEATURES	Source	1. 617	/organism="Homo sapiens"	/db_xref="taxon:9606"	/clone="IMAGE:3628580"	/clone_lib="NIH_MGC_19"	/tissue_type="neuroblastoma"	/lab_host="DH10B (phage-resistant)"	/note="Organ: Brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(5). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC Library."
BASE COUNT	130 a	193 c	178 g	116 t					
ORIGIN									
Query Match	46.8%	Score 502:	DB 10:	Length 617:					
Best Local Similarity	99.7%	Pred. NO. 5.6e-248:							
Matches 602:	Conservative	0:	Mismatches 2:	Indels	0:	Gaps			
46	AGCGGCGTGGCTGCTCTCTGTGGGTGGCGGCTCGGCGCAGACAGACGAGACTTTCACGA	105							
14	AGCGGCGTGGCTGCTCTCTGTGGGTGGCGGCTCGGCGCAGACAGACGAGACTTTCACGA	73							
106	CTTCAAGGCGGTCAACATCCGGGGCAACATGCTGTGCTGTGGAGAGTACCGCGGATCGGT	165							
74	CTTCAAGGCGGTCAACATCCGGGGCAACATGCTGTGCTGTGGAGAGTACCGCGGATCGGT	133							
166	GTCCTGGTGTGTAATGTGGCGACAGAGTGCAGGTTTACAGACAGACATCAGGACCCCT	225							
134	GTCCTGGTGTGTAATGTGGCGACAGAGTGCAGGTTTACAGACAGACATCAGGACCCCT	193							
226	GCAGCAGCTGCAGCAGACCTGGGCCCCCACCACACTTCAAGCTGCTGGCTTCCCTGCAA	285							
194	GCAGCAGCTGCAGCAGACCTGGGCCCCCACCACACTTCAAGCTGCTGGCTTCCCTGCAA	253							
286	CCAGTTTGGCCCAAGAGAGCGCTGACACACCAAGAGATGAGAGCTTTGCCCTCCGCAC	345							
254	CCAGTTTGGCCCAAGAGAGCGCTGACACCAAGAGATGAGAGCTTTGCCCTCCGCAC	313							
346	CTACAGTGTCTCATTTCCCATGTTTACCAAGATTGTCAGTACCGGTACTGTGCCATCC	405							
314	CTACAGTGTCTCATTTCCCATGTTTACCAAGATTGTCAGTACCGGTACTGTGCCATCC	373							
406	TGCCTTCAAGTACTGGCCCAAGCTTTGGGAGAGAGCCACCTGGAACTTGTGAAGTA	465							
374	TGCCTTCAAGTACTGGCCCAAGCTTTGGGAGAGAGCCACCTGGAACTTGTGAAGTA	433							

OY	466	CCTGTATACCCACAGATGGAAAGTGATGAGGGGCTTGGACACCACTGTGTAGTGGAGGA	525
OY	434	CCTGTATACCCACAGATGGAAAGTGATGAGGGGCTTGGACACCACTGTGTAGTGGAGGA	493
OY	526	GGTAGACTCCAGATTCACAGCGCTCGTAGAGAGACTCATCTACTAGAACGAGAAGACTT	585
Db	494	GGTCAGACCCACAGATTCACAGCGCTCGTAGAGAGACTCATCTACTAGAACGAGAAGACTT	553
OY	586	ATAACACCGCGGTCTCTCTCTCCACACACTTATCCCGCCACCTGTGTGTGGGGCTGACCA	645
Db	554	ATAACACCGCGGTCTCTCTCTCCACACACTTATCCCGCCACCTGTGTGTGGGGCTGACCA	613
OY	646	TGCA	649
Db	614	TGCA	617
RESULT	7		
LOCUS	AA406605/c		
DEFINITION	AA406605	519 bp	mRNA
ACCESSION	ZV15B04.S1 Soares_NhHMPU_S1	Human sapiens	CDNA clone IMAGE:753679
VERSION	AA406605		
KEYWORDS	AA406605.1 GI:2064615		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 519) Hillier, L., Allen, M., Bowles, L., Dubnue, T., Giesel, G., Jost, S., Kucab, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997 Unpublished (1997) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: -41m3 fwd. ER from Amersham High quality sequence stop: 461. Location/Qualifiers		
FEATURES	source		
	1..519		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:753679"		
	/clone_id="Soares_NhHMPU_S1"		
	/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"		
	/lab_host="DH10B"		
	/note="Organ: mixed (see below); Vector: p773D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbH, pregnant uterus NbH, and fetal heart NbH19M) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."		
BASE COUNT	131 a	100 c	126 g 162 t
ORIGIN			
Query Match	43.7%	Score 468;	DB 9; Length 519;





RESULT	11
LOCUS	B1561449
DEFINITION	B1561449 846 bp mRNA linear EST 05-SEP-2001 60323613JF1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:5298607 5' , mRNA sequence.
ACCESSION	B1561449
VERSION	B1561449.1 GI:15448763
KEYWORDS	EST .
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 846) NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Robert Strausberg, Ph.D.
TITLE	
JOURNAL	
COMMENT	

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA library preparation: Michael J. Brownstein (NHGRI), Shiroaki  
Toshitoki and Piero Carninci (RIKEN)  
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM1175 row: m column: 08  
High quality sequence spot: 842.

FEATURES	Location/Qualifiers
source	1. .846

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SOURCE
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/db_xref="taxon:9606"
/clone="IMAGE:5298607"
/clone_1ib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagc
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to R07 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT
194 a 244 c 232 g 175 t 1 others

```

Query Match	40.8%;	Score 437;	DB 10;	Length 846;
Best Local Similarity	-99.5%;	Pred. No. 2.2e-214;		
Matches 587;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

QY	19	ACAGCCATGGTGGCGCGAGAGGTGGGACGGCGCGTGGCTCTCTCTGGGCTCGCGCTG	78
Db	9	ACAAACCCATGGTGGGGGGGAGCGTGGGACGGCGCGCTGGCTCTCTGTGGGCTCGGCGCTG	68
QY	79	CGCGAGCAGAGGACGAGCACTTCTACGACTTCAAGCGCGTCAACATCCGGGGCAAACTGTT	138
Db	69	CGCGAGCAGGAGGACGAGCACTTCTACGACTTCAAGCGCGTCAACATCCGGGGCAAACTGTT	128
QY	139	GTGCGTGGAGAAATACCCGGGATGGGTGTCCCTGTGTGTAAATGTGGCCAGCGAGTGGG	198
Db	129	ATCGGTGGGAGAGTACCGCGGATGGGTGTCCCTGTGTGTAAATGTGGCCAGCGAGTGGG	188
QY	199	CTTCAACAGACGACACTACGAGCCCTGACACAGCTGACGAGGAGCACTTGGGCCCCACCA	258
Db	189	CTTCAACAGACGACACTACGAGCCCTGACACAGCTGAGGAGCACTTGGGCCCCACCA	248
QY	259	CTTCAACGCTGCTGCCCTTCCCTGCAACCACTTTGGCCACAGGAGGCTGACAGCAACAA	318
Db	249	CTTCAACGCTGCTGCCCTTCCCTGCAACCACTTTGGCCACAGGAGGCTGACAGCAACAA	308

QY	319	GGAGATTGAGACCTTTGGCTGCCGACCTAACGATGTCATTCCCATGTTAGCAAT	378
Db	309	GGAGATTGAGACCTTTGGCCCGCGACCTACAGTGTCTCATTTCCCATGTTAGCAAT	368
QY	379	TGCACCTCACCGGTACTGTTGTCATCTGTCCTTCAAGTACCTGGCCGACCTTCTGGAA	438
Db	369	TGCACCTCACCGGTACTGTTGTCATCTGTCCTTCAAGTACCTGGCCGACCTTCTGGAA	428
QY	439	GGAGCCCACTGGACCTCTGSAATTAAGTATGACCCAGATGGAAAGGTGTGGGC	498
Db	429	GGAGCCCACTGGAACTCTGSAATTAAGTATGACCCAGATGGAAAGGTGTGGGC	488
QY	499	TTGGGACCCAACTGTGTAGTGGAGAGGTCAGACTCAGATCACAGCGCTGTGAGAA	558
Db	489	TTGGGACCCAACTGTGTAGTGGAGAGGTCAGACCCAGATCACAGCGCTGTGAGAA	548
QY	559	GCTCATCTCACTGAAAGCGGAGAGACTTTAAACACCGGCTCTCTCTCC	608
Db	549	GCTCATCTCACTGAAAGCGGAGAGACTTTAAACACCGGCTCTCTCTCTCC	598

[illegible]

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 465)  
REFERENCE  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE

JOURNAL  
COMMENT

Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert length: 1075 std error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 453.

## FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:2449158"
/clone_1ib="NCI-CCAP-Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
metastatic)"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pRT73d-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
pooled lung tumor tissue, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the NotI and Eco RI sites of the modified
pRT73 vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.
Fatima Bonaldo."

```



Query Match 39.1%; Score 419; DB 9; Length 465;  
Best Local Similarity 100.0%; Pred. No. 4.2e-205;  
Matches 419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 CTCACACACCTATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGTGCT 664  
DB 461 CTCACACACCTATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGTGCT 402  
QY 665 TCAAAAGGAGAGACCCACTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 724  
DB 401 TCAAAAGGAGAGACCCACTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 342  
QY 725 CTGTGGGGGAAAAATTTAGTATTTTGTATTTGATTTGATTTGATTTGATTTGATTT 784  
DB 341 CTGTGGGGGAAAAATTTAGTATTTTGTATTTGATTTGATTTGATTTGATTTGATTT 282  
QY 785 TCTGTGGCCATGAGAGCTCTTGTACCAAGTACACAGCCGATACAGCTCTTGTCCAC 844  
DB 281 TCTGTGGCCATGAGAGCTCTTGTACCAAGTACACAGCCGATACAGCTCTTGTCCAC 222  
QY 845 AAAAATGTGTGCAATATGAGTATATCAAGCAATATCTCCACCCCAAGCTTGTGTA 904  
DB 221 AAAAATGTGTGCAATATGAGTATATCAAGCAATATCTCCACCCCAAGCTTGTGTA 162  
QY 905 ACTGGGACCAATGATTAATCTCATAGGGCTGTGTGAGATTTGATTAATTAATCTGTGA 964  
DB 161 ACTGGGACCAATGATTAATCTCATAGGGCTGTGTGAGATTTGATTAATTAATCTGTGA 102  
QY 965 AGTGCCTAGGACAGTGCACGCCAATATGAGAGCAATTCATGAACATTTTGTGATATAA 1023  
DB 101 AGTGCCTAGGACAGTGCACGCCAATATGAGAGCAATTCATGAACATTTTGTGATATAA 43

RESULT 13  
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LOCUS UI-HF-BL0-adb-c-12-0-UI.s1 NIH\_MGC\_37 Homo sapiens cDNA clone  
DEFINITION IMAGE:3060886 3', mRNA sequence.  
ACCESSION AM576111.1 GI:7247650  
VERSION AM576111.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 464)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A,  
tail. Tissue Procurement: Louis M. Staedt, M.D., Ph.D.  
cDNA Library Preparation: Louis M. Staedt, M.D., Ph.D.  
cDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
www.bio.lnl.gov/bbrp/image/image.html  
The following repetitive elements were found in this cDNA  
sequence:  
65-181, >MIR  
Seq Primer: M13 Forward  
POLYA=Yes.  
Location/Qualifiers  
1. 464  
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/clone="IMAGE:3060886"

/clone="NIH\_MGC\_37"  
/tissue\_type="Lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (UTI)"  
/note="Vector: p7773-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staedt, Ph.D. Library preparation by Maria de Fatima  
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 117 a 88 c 101 g 158 t

Query Match 38.2%; Score 409; DB 9; Length 464;  
Best Local Similarity 100.0%; Pred. No. 6.1e-200;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 TCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGTGCTTCAAGGAG 674  
DB 464 TCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGTGCTTCAAGGAG 405  
QY 675 AGACCACTGACT 734  
DB 404 AGACCACTGACT 345  
QY 735 AAAAATTTAGTATTTTGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 794  
DB 344 AAAAATTTAGTATTTTGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 285  
QY 795 TGAGAGCTCTTGTACCAAGTACACAGCCGATACAGCTCTTGTCCCAACAAATGTGT 854  
DB 284 TGAGAGCTCTTGTACCAAGTACACAGCCGATACAGCTCTTGTCCCAACAAATGTGT 225  
QY 855 GGCAAATATGAGTATATCAAGCAATATCTCCACCCCAAGCTTGTATATCTGGAGCA 914  
DB 224 GGCAAATATGAGTATATCAAGCAATATCTCCACCCCAAGCTTGTATATCTGGAGCA 165  
QY 915 ATGATTATTCATATGAGGCTGTGTGAGATTTGATTAATTAATCTGTGAAAGTCCAGG 974  
DB 164 ATGATTATTCATATGAGGCTGTGTGAGATTTGATTAATTAATCTGTGAAAGTCCAGG 105  
QY 975 CAGTGCACGCCAATATGAGAGCAATTCATGAACATTTTGTGATATAA 1023  
DB 104 CAGTGCACGCCAATATGAGAGCAATTCATGAACATTTTGTGATATAA 56

RESULT 14  
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LOCUS ag35b03.s1 jia bone marrow stroma Homo sapiens cDNA clone  
DEFINITION IMAGE:1091501 3', mRNA sequence.  
ACCESSION AA599283  
VERSION AA599283.1 GI:2432908  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 456)  
AUTHORS Jia, L., Robey, P., Young, M., Schuler, G., Powell, J., Yang, L., Lennon  
G., Hillier, L., Allen, M., Bowles, L., Geisler, S., Kucaba, T., Marra  
M., Martin, J., Stepien, M., Tan, F., Theising, B., Bowers, Y., Wylie  
T., Waterston, R., Wilson, R. and Francomano, C.  
WashU-MGB/NHGRI EST Project  
Unpublished (1997)  
Contact: Wilson RK / Jia L  
WashU-MGB/NHGRI EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estelwatson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 1191 Std Error: 0.00  
Seq primer: -40m13 fwd. ER from Amersham  
High quality sequence stop: 447.

FEATURES

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/sex="mixed"  
/tissue\_type="bone marrow stroma"  
/dev\_stage="mixed"  
/lab\_host="XLI-Blue MRF/SOLR"  
/note="Vector: pBluescript; Site\_1: EcoRI; Site\_2: XhoI;  
mRNA made from human bone marrow stroma, cDNA made by  
oligo-dT priming. Directionally cloned. Size-selected for  
average insert size >0.5 kb. Library supplied by Dr. libin  
Jia (NHGRI)."  
BASE COUNT 117 a 89 c 106 g 144 t  
ORIGIN

Query Match 37.7%; Score 404; DB 9; Length 456;  
Best Local Similarity 99.8%; Pred. No. 2.3e-197;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 608 CACCACTCCTATCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGGTCTTCA 667  
|||||  
DB 456 CACCACTCCTATCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGGTCTTCA 397  
OY 668 AAGGAGAGACCCAGTCT 727  
|||||  
DB 36 AAGGAGAGACCCAGTCT 337  
OY 728 GTGGGGGAAAAATTTCTAGTATTTTGTATTTTGAATCTTACAGCAACAATAGGAAGTCC 787  
|||||  
DB 336 GTGGGGGAAAAATTTCTAGTATTTTGTATTTTGAATCTTACAGCAACAATAGGAAGTCC 277  
OY 788 TGGCCCAATGAGAGCTCTTACCAAGTAAATCAGCCAGCCGATAGCAAGCTTGGCAACAA 847  
|||||  
DB 276 TGGCCCAATGAGAGCTCTTACCAAGTAAATCAGCCAGCCGATAGCAAGCTTGGCAACAA 217  
OY 848 AATGTGTGCAATAGAAATATATATCAAGCAATATCTCCACCCAGGCTTGTGTAATCT 907  
|||||  
DB 216 AATGTGTGCAATAGAAATATATATCAAGCAATATCTCCACCCAGGCTTGTGTAATCT 157  
OY 908 GAGACCAATGATTTACCTCATAGGGCTGTGTGAGATTTAGATGAATACCTGTGAAGT 967  
|||||  
DB 156 GAGACCAATGATTTACCTCATAGGGCTGTGTGAGATTTAGATGAATACCTGTGAAGT 97  
OY 968 GCGTAGGCGTGGCAGCAGCAATAGAGGAGCATTCATGAACATTTTGGCATATAACCAA 1027  
|||||  
DB 96 GCGTAGGCGTGGCAGCAGCAATAGAGGAGCATTCATGAACATTTTGGCATATAACCAA 37  
OY 1028 AAAATTAATCTTTATCAATAAAACTTGATCCAA 1062  
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DB 36 AAAATTAATCTTTATCAATAAAACTTGATCCAA 2

RESULT 15  
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LOCUS AI332841/c  
DEFINITION gp96g11.x1 Soares\_fetal\_lung NBHL19W Homo sapiens cDNA clone  
IMAGE:1930916 3', mRNA sequence.  
ACCESSION AI332841  
VERSION AI332841.1 GI:4069400  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 466)  
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 1446 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 394.

FEATURES

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/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
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strand cDNA was primed with a Not I - oligo(dT) primer  
[5'-GTGACCAATCTGAAGTGGAGGCGGCGCAATTTTGTGTTTGT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pTZ19 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M. Palma Bonaldo. This library was constructed  
from the same fetus as the fetal heart library, Soares  
fetal heart NBHL19W."  
BASE COUNT 122 a 91 c 102 g 151 t  
ORIGIN

Query Match 37.3%; Score 400; DB 9; Length 466;  
Best Local Similarity 100.0%; Pred. No. 2.7e-195;  
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 624 CCACCTGTGGGGGCTGACCAATGCAAACTCAATAGTGTCTCAAGGAGAGACCCACT 683  
|||||  
DB 466 CCACCTGTGGGGGCTGACCAATGCAAACTCAATAGTGTCTCAAGGAGAGACCCACT 407  
OY 684 GACTTCCTCTCTTACTCTTATGACATTTGTCATCATTTCTTGTGGGGAAAAATTCCT 743  
|||||  
DB 406 GACTTCCTCTCTTACTCTTATGACATTTGTCATCATTTCTTGTGGGGAAAAATTCCT 347  
OY 744 AGTATTTTGTATTTTGAATCTTACAGCAACAATAGGAAGCTCTGCCAATGAGAGCTC 803  
|||||  
DB 346 AGTATTTTGTATTTTGAATCTTACAGCAACAATAGGAAGCTCTGCCAATGAGAGCTC 287  
OY 804 TTGACCAATGCAATCAGCAGCGATAGCAAGCTTTCGCAACAATAATGTGTGCAATAG 863  
|||||  
DB 286 TTGACCAATGCAATCAGCAGCGATAGCAAGCTTTCGCAACAATAATGTGTGCAATAG 227  
OY 864 AAGTATATCAAGCAATATCTCCACCCAGGCTTGTGTAATCTGGGACCAATGATTTACC 923  
|||||  
DB 226 AAGTATATCAAGCAATATCTCCACCCAGGCTTGTGTAATCTGGGACCAATGATTTACC 167  
OY 924 TCATAGGCGTGTGAGAGTTAGAGTAATACCTGTGAAGTGGCTAGGCGAGTGGCAG 983  
|||||  
DB 166 TCATAGGCGTGTGAGAGTTAGAGTAATACCTGTGAAGTGGCTAGGCGAGTGGCAG 107  
OY 984 CCAATATAGAGGCAATCAATGATGATTTTGGCATATAA 1023  
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DB 106 CCAATATAGAGGCAATCAATGATGATTTTGGCATATAA 67

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Job time: 5379 sec

Mon Aug 26 08:01:43 2002

us-09-811-118-2.01i.rst

Page 11

